

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/530,837  
Source: PGT/10  
Date Processed by STIC: 4/19/05

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 04/19/2005

PATENT APPLICATION: US/10/530,837

TIME: 08:43:24

Input Set : A:\LL05US001.txt

Output Set: N:\CRF4\04192005\J530837.raw

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1 <110> APPLICANT: LG Life Sciences Ltd.
3 <120> TITLE OF INVENTION: Gene Famililies Associated With Cancers
5 <130> FILE REFERENCE: LL03PCT006
C--> 7 <140> CURRENT APPLICATION NUMBER: US/10/530,837
C--> 7 <141> CURRENT FILING DATE: 2005-04-08
7 <150> PRIOR APPLICATION NUMBER: US60/419911
8 <151> PRIOR FILING DATE: 2002-10-18
10 <150> PRIOR APPLICATION NUMBER: US60/419912
11 <151> PRIOR FILING DATE: 2002-10-18
13 <150> PRIOR APPLICATION NUMBER: US60/420088
14 <151> PRIOR FILING DATE: 2002-10-18
16 <150> PRIOR APPLICATION NUMBER: US60/434243
17 <151> PRIOR FILING DATE: 2002-12-16
19 <150> PRIOR APPLICATION NUMBER: US60/434278
20 <151> PRIOR FILING DATE: 2002-12-16
22 <150> PRIOR APPLICATION NUMBER: US60/438278
23 <151> PRIOR FILING DATE: 2003-01-03
25 <160> NUMBER OF SEQ ID NOS: 56
27 <170> SOFTWARE: KopatentIn 1.71
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 5293
31 <212> TYPE: DNA
32 <213> ORGANISM: Homo sapiens
34 <220> FEATURE:
35 <221> NAME/KEY: CDS
36 <222> LOCATION: (390)..(4880)
37 <223> OTHER INFORMATION: LBFL109 Clone A
40 <400> SEQUENCE: 1
41 gtcctgtctg gcggtgccga cgggtgagggg cgggtggccca acggcgaggag attcaaacct      60
43 ggaagaagga ggaacatgga gaggagagca gcgggcccag gctgggcagc ctctggatcg      120
45 aggcctgcct gaaggaggag cttccttccc cgggtggagct ggaggagagc cttcggaatg      180
47 gagtgcctgt ggccaagctg ggccactggt ttgcaccctc cgtgggtccg ttgaagaaga      240
49 tctacgatgt ggagcagctg cgggtaccagg caactggctt acatttcggt cacacagaca      300
51 acatcaactt ttggctatct gcaatagccc acatcgggtc gccttcgacc ttcttcccag      360
53 agaccacgga catctatgac aaaaagaac atg ccc cgg gta gtc tac tgc atc      413
54                               Met Pro Arg Val Val Tyr Cys Ile
55                               1                               5
57 cat gct ctc agt ctc ttc ctc ttc cgg ctg gga ttg gcc cct cag ata      461
58 His Ala Leu Ser Leu Phe Leu Phe Arg Leu Gly Leu Ala Pro Gln Ile
59   10                               15                               20
61 cat gat cta tac ggg aaa gtg aaa ttc aca gct gag gaa ctc agc aac      509
62 His Asp Leu Tyr Gly Lys Val Lys Phe Thr Ala Glu Glu Leu Ser Asn
63 25                               30                               35                               40

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65	atg	gcg	tcc	gaa	ctg	gcc	aaa	tat	ggc	ctc	cag	ctg	cct	gcc	ttc	agc	557
66	Met	Ala	Ser	Glu	Leu	Ala	Lys	Tyr	Gly	Leu	Gln	Leu	Pro	Ala	Phe	Ser	
67				45					50					55			
69	aag	atc	ggg	ggc	atc	ttg	gcc	aat	gag	ctc	tcg	gtg	gat	gag	gct	gca	605
70	Lys	Ile	Gly	Gly	Ile	Leu	Ala	Asn	Glu	Leu	Ser	Val	Asp	Glu	Ala	Ala	
71			60					65				70					
73	gtc	cat	gca	gct	gtt	ctt	gcc	atc	aat	gaa	gca	gtg	gag	cga	ggg	gtg	653
74	Val	His	Ala	Ala	Val	Leu	Ala	Ile	Asn	Glu	Ala	Val	Glu	Arg	Gly	Val	
75			75					80				85					
77	gtg	gag	gac	acc	ctg	gct	gcc	ttg	cag	aat	ccc	agt	gct	ctt	ctg	gag	701
78	Val	Glu	Asp	Thr	Leu	Ala	Ala	Leu	Gln	Asn	Pro	Ser	Ala	Leu	Leu	Glu	
79		90					95				100						
81	aat	ctc	cga	gag	cct	ctg	gca	gcc	gtc	tac	cag	gag	atg	ctg	gcc	cag	749
82	Asn	Leu	Arg	Glu	Pro	Leu	Ala	Ala	Val	Tyr	Gln	Glu	Met	Leu	Ala	Gln	
83	105				110					115				120			
85	gcc	aag	atg	gag	aag	gca	gcc	aat	gcc	agg	aac	cat	gat	gac	aga	gaa	797
86	Ala	Lys	Met	Glu	Lys	Ala	Ala	Asn	Ala	Arg	Asn	His	Asp	Asp	Arg	Glu	
87			125						130			135					
89	agc	cag	gac	atc	tat	gac	cac	tac	cta	act	cag	gct	gaa	atc	cag	ggc	845
90	Ser	Gln	Asp	Ile	Tyr	Asp	His	Tyr	Leu	Thr	Gln	Ala	Glu	Ile	Gln	Gly	
91			140					145				150					
93	aat	atc	aac	cat	gtc	aac	gtc	cat	ggg	gct	cta	gaa	gtt	gtt	gat	gat	893
94	Asn	Ile	Asn	His	Val	Asn	Val	His	Gly	Ala	Leu	Glu	Val	Val	Asp	Asp	
95		155					160				165						
97	gcc	ctg	gaa	aga	cag	agc	cct	gaa	gcc	ttg	ctc	aag	gcc	ctt	caa	gac	941
98	Ala	Leu	Glu	Arg	Gln	Ser	Pro	Glu	Ala	Leu	Leu	Lys	Ala	Leu	Gln	Asp	
99		170				175				180							
101	cct	gcc	ctg	gcc	ctg	cga	ggg	gtg	agg	aga	gac	ttt	gct	gac	tgg	tac	989
102	Pro	Ala	Leu	Ala	Leu	Arg	Gly	Val	Arg	Arg	Asp	Phe	Ala	Asp	Trp	Tyr	
103	185				190					195				200			
105	ctg	gag	cag	ctg	aac	tca	gac	aga	gag	cag	aag	gca	cag	gag	ctg	ggc	1037
106	Leu	Glu	Gln	Leu	Asn	Ser	Asp	Arg	Glu	Gln	Lys	Ala	Gln	Glu	Leu	Gly	
107			205					210			215						
109	ctg	gtg	gag	ctt	ctg	gaa	aag	gag	gaa	gtc	cag	gct	ggt	gtg	gct	gca	1085
110	Leu	Val	Glu	Leu	Leu	Glu	Lys	Glu	Glu	Val	Gln	Ala	Gly	Val	Ala	Ala	
111			220					225			230						
113	gcc	aac	aca	aag	ggt	gat	cag	gaa	caa	gcc	atg	ctc	cac	gct	gtg	cag	1133
114	Ala	Asn	Thr	Lys	Gly	Asp	Gln	Glu	Gln	Ala	Met	Leu	His	Ala	Val	Gln	
115		235				240				245							
117	cgg	atc	aac	aaa	gcc	atc	cgg	agg	gga	gtg	gcg	gct	gac	act	gtg	aag	1181
118	Arg	Ile	Asn	Lys	Ala	Ile	Arg	Arg	Gly	Val	Ala	Ala	Asp	Thr	Val	Lys	
119		250				255				260							
121	gag	ctg	atg	tgc	cct	gag	gcc	cag	ctg	cct	cca	gtg	tac	cct	gtt	gca	1229
122	Glu	Leu	Met	Cys	Pro	Glu	Ala	Gln	Leu	Pro	Pro	Val	Tyr	Pro	Val	Ala	
123	265				270				275			280					
125	tcg	tct	atg	tac	cag	ctg	gag	ctg	gca	gtg	ctc	cag	cag	cag	cag	ggg	1277
126	Ser	Ser	Met	Tyr	Gln	Leu	Glu	Leu	Ala	Val	Leu	Gln	Gln	Gln	Gln	Gly	
127			285					290			295						
129	gag	ctt	ggc	cag	gag	gag	ctc	ttc	gtg	gct	gtg	gag	atg	ctc	tca	gct	1325

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130	Glu	Leu	Gly	Gln	Glu	Glu	Leu	Phe	Val	Ala	Val	Glu	Met	Leu	Ser	Ala	
131				300					305					310			
133	gtg	gtc	ctg	att	aac	cgg	gcc	ctg	gag	gcc	cgg	gat	gcc	agt	ggc	ttc	1373
134	Val	Val	Leu	Ile	Asn	Arg	Ala	Leu	Glu	Ala	Arg	Asp	Ala	Ser	Gly	Phe	
135			315					320					325				
137	tgg	agc	agc	ctg	gtg	aac	cct	gcc	aca	ggc	ctg	gct	gag	gtg	gaa	gga	1421
138	Trp	Ser	Ser	Leu	Val	Asn	Pro	Ala	Thr	Gly	Leu	Ala	Glu	Val	Glu	Gly	
139		330					335					340					
141	gaa	aat	gcc	cag	cgt	tac	ttc	gat	gcc	ctg	ctg	aaa	ttg	cga	cag	gag	1469
142	Glu	Asn	Ala	Gln	Arg	Tyr	Phe	Asp	Ala	Leu	Leu	Lys	Leu	Arg	Gln	Glu	
143	345					350					355					360	
145	cgt	ggg	atg	ggt	gag	gac	ttc	ctg	agc	tgg	aat	gac	ctg	cag	gcc	acc	1517
146	Arg	Gly	Met	Gly	Glu	Asp	Phe	Leu	Ser	Trp	Asn	Asp	Leu	Gln	Ala	Thr	
147				365					370					375			
149	gtg	agc	cag	gtc	aat	gca	cag	acc	cag	gaa	gag	act	gac	cgg	gtc	ctt	1565
150	Val	Ser	Gln	Val	Asn	Ala	Gln	Thr	Gln	Glu	Glu	Thr	Asp	Arg	Val	Leu	
151			380						385					390			
153	gca	gtc	agc	ctc	atc	aat	gag	gct	ctg	gac	aaa	ggc	agc	cct	gag	aag	1613
154	Ala	Val	Ser	Leu	Ile	Asn	Glu	Ala	Leu	Asp	Lys	Gly	Ser	Pro	Glu	Lys	
155		395					400						405				
157	act	ctg	tct	gcc	cta	ctg	ctt	cct	gca	gct	ggc	cta	gat	gat	gtc	agc	1661
158	Thr	Leu	Ser	Ala	Leu	Leu	Leu	Pro	Ala	Ala	Gly	Leu	Asp	Asp	Val	Ser	
159		410				415					420						
161	ctc	cct	gtc	gcc	cct	cgg	tac	cat	ctc	ctc	ctt	gtg	gca	gcc	aaa	agg	1709
162	Leu	Pro	Val	Ala	Pro	Arg	Tyr	His	Leu	Leu	Leu	Val	Ala	Ala	Lys	Arg	
163	425				430				435							440	
165	cag	aag	gcc	cag	gtg	aca	ggg	gat	cct	gga	gct	gtg	ctg	tgg	ctt	gag	1757
166	Gln	Lys	Ala	Gln	Val	Thr	Gly	Asp	Pro	Gly	Ala	Val	Leu	Trp	Leu	Glu	
167			445					450						455			
169	gag	atc	cgc	cag	gga	gtg	gtc	aga	gcc	aac	cag	gac	act	aat	aca	gct	1805
170	Glu	Ile	Arg	Gln	Gly	Val	Val	Arg	Ala	Asn	Gln	Asp	Thr	Asn	Thr	Ala	
171			460					465					470				
173	cag	aga	atg	gct	ctt	ggt	gtg	gct	gcc	atc	aat	caa	gcc	atc	aag	gag	1853
174	Gln	Arg	Met	Ala	Leu	Gly	Val	Ala	Ala	Ile	Asn	Gln	Ala	Ile	Lys	Glu	
175		475				480						485					
177	ggc	aag	gca	gcc	cag	act	gag	cgg	gtg	ttg	agg	aac	ccc	gca	gtg	gcc	1901
178	Gly	Lys	Ala	Ala	Gln	Thr	Glu	Arg	Val	Leu	Arg	Asn	Pro	Ala	Val	Ala	
179		490				495					500						
181	ctt	cga	ggg	gta	gtt	ccc	gac	tgt	gcc	aac	ggc	tac	cag	cga	gcc	ctg	1949
182	Leu	Arg	Gly	Val	Val	Pro	Asp	Cys	Ala	Asn	Gly	Tyr	Gln	Arg	Ala	Leu	
183	505				510						515					520	
185	gaa	agt	gcc	atg	gca	aag	aaa	cag	cgt	cca	gca	gac	aca	gct	ttc	tgg	1997
186	Glu	Ser	Ala	Met	Ala	Lys	Lys	Gln	Arg	Pro	Ala	Asp	Thr	Ala	Phe	Trp	
187			525					530						535			
189	gtt	caa	cat	gac	atg	aag	gat	ggc	act	gcc	tac	tac	ttc	cat	ctg	cag	2045
190	Val	Gln	His	Asp	Met	Lys	Asp	Gly	Thr	Ala	Tyr	Tyr	Phe	His	Leu	Gln	
191			540					545					550				
193	acc	ttc	cag	ggg	atc	tgg	gag	caa	cct	cct	ggc	tgc	ccc	ctc	aac	acc	2093
194	Thr	Phe	Gln	Gly	Ile	Trp	Glu	Gln	Pro	Pro	Gly	Cys	Pro	Leu	Asn	Thr	

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195	555	560	565	
197 tct cac ctg acc cgg gag gag atc cag tca gct gtc acc aag gtc act				2141
198 Ser His Leu Thr Arg Glu Glu Ile Gln Ser Ala Val Thr Lys Val Thr				
199 570	575	580		
201 gct gcc tat gac cgc caa cag ctc tgg aaa gcc aac gtc ggc ttt gtt				2189
202 Ala Ala Tyr Asp Arg Gln Gln Leu Trp Lys Ala Asn Val Gly Phe Val				
203 585	590	595	600	
205 atc cag ctc cag gcc cgc ctc cgt ggc ttc cta gtt cgg cag aag ttt				2237
206 Ile Gln Leu Gln Ala Arg Leu Arg Gly Phe Leu Val Arg Gln Lys Phe				
207 605	610	615		
209 gct gag cat tcc cac ttt ctg agg acc tgg ctc cca gca gtc atc aag				2285
210 Ala Glu His Ser His Phe Leu Arg Thr Trp Leu Pro Ala Val Ile Lys				
211 620	625	630		
213 atc cag gct cat tgg cgg ggt tat agg cag cgg aag att tac ctg gag				2333
214 Ile Gln Ala His Trp Arg Gly Tyr Arg Gln Arg Lys Ile Tyr Leu Glu				
215 635	640	645		
217 tgg ttg cag tat ttt aaa gca aac ctg gat gcc ata atc aag atc cag				2381
218 Trp Leu Gln Tyr Phe Lys Ala Asn Leu Asp Ala Ile Ile Lys Ile Gln				
219 650	655	660		
221 gcc tgg gcc cgg atg tgg gca gct cgg agg caa tac ctg agg cgt ctg				2429
222 Ala Trp Ala Arg Met Trp Ala Ala Arg Arg Gln Tyr Leu Arg Arg Leu				
223 665	670	675	680	
225 cac tac ttc cag aag aat gtt aac tcc att gtg aag atc cag gca ttt				2477
226 His Tyr Phe Gln Lys Asn Val Asn Ser Ile Val Lys Ile Gln Ala Phe				
227 685	690	695		
229 ttc cga gcc agg aaa gcc caa gat gac tac agg ata tta gtg cat gca				2525
230 Phe Arg Ala Arg Lys Ala Gln Asp Asp Tyr Arg Ile Leu Val His Ala				
231 700	705	710		
233 ccc cac cct cct ctc agt gtg gta cgc aga ttt gcc cat ctc ttg aat				2573
234 Pro His Pro Pro Leu Ser Val Val Arg Arg Phe Ala His Leu Leu Asn				
235 715	720	725		
237 caa agc cag caa gac ttc ttg gct gag gca gag ctg ctg aag ctc cag				2621
238 Gln Ser Gln Gln Asp Phe Leu Ala Glu Ala Glu Leu Leu Lys Leu Gln				
239 730	735	740		
241 gaa gag gta gtt agg aag atc cga tcc aat cag cag ctg gag cag gac				2669
242 Glu Glu Val Val Arg Lys Ile Arg Ser Asn Gln Leu Glu Gln Asp				
243 745	750	755	760	
245 ctc aac atc atg gac atc aag att ggc ctg ctg gtg aag aac cgg atc				2717
246 Leu Asn Ile Met Asp Ile Lys Ile Gly Leu Leu Val Lys Asn Arg Ile				
247 765	770	775		
249 act ctg cag gaa gtg gtc tcc cac tgc aag aag ctg acc aag agg aat				2765
250 Thr Leu Gln Glu Val Val Ser His Cys Lys Lys Leu Thr Lys Arg Asn				
251 780	785	790		
253 aag gaa cag ctg tca gat atg atg gtt ctg gac aag cag aag ggt tta				2813
254 Lys Glu Gln Leu Ser Asp Met Met Val Leu Asp Lys Gln Lys Gly Leu				
255 795	800	805		
257 aag tcg ctg agc aaa gag aaa cgg cag aaa cta gaa gca tac caa cac				2861
258 Lys Ser Leu Ser Lys Glu Lys Arg Gln Lys Leu Glu Ala Tyr Gln His				
259 810	815	820		

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261	ctc	ttc	tac	ctg	ctc	cag	act	cag	ccc	atc	tac	ctg	gcc	aag	ctg	atc	2909
262	Leu	Phe	Tyr	Leu	Leu	Gln	Thr	Gln	Pro	Ile	Tyr	Leu	Ala	Lys	Leu	Ile	
263	825					830					835					840	
265	ttt	cag	atg	cca	cag	aac	aaa	acc	acc	aag	ttc	atg	gag	gca	gtg	att	2957
266	Phe	Gln	Met	Pro	Gln	Asn	Lys	Thr	Thr	Lys	Phe	Met	Glu	Ala	Val	Ile	
267					845					850						855	
269	ttc	agc	ctg	tac	aac	tat	gcc	tcc	agc	cgc	cga	gag	gcc	tat	ctc	ctg	3005
270	Phe	Ser	Leu	Tyr	Asn	Tyr	Ala	Ser	Ser	Arg	Arg	Glu	Ala	Tyr	Leu	Leu	
271					860					865						870	
273	ctc	cag	ctg	ttc	aag	aca	gca	ctc	cag	gag	gaa	atc	aag	tca	aag	gtg	3053
274	Leu	Gln	Leu	Phe	Lys	Thr	Ala	Leu	Gln	Glu	Glu	Ile	Lys	Ser	Lys	Val	
275					875					880						885	
277	gag	cag	ccc	cag	gac	gtg	gtg	aca	ggc	aac	cca	aca	gtg	gtg	agg	ctg	3101
278	Glu	Gln	Pro	Gln	Asp	Val	Val	Thr	Gly	Asn	Pro	Thr	Val	Val	Arg	Leu	
279					890					895						900	
281	gtg	gtg	aga	ttc	tac	cgt	aat	ggg	cgg	gga	cag	agt	gcc	ctg	cag	gag	3149
282	Val	Val	Arg	Phe	Tyr	Arg	Asn	Gly	Arg	Gly	Gln	Ser	Ala	Leu	Gln	Glu	
283	905					910					915					920	
285	att	ctg	ggc	aag	gtt	atc	cag	gat	gtg	cta	gaa	gac	aaa	gtg	ctc	agc	3197
286	Ile	Leu	Gly	Lys	Val	Ile	Gln	Asp	Val	Leu	Glu	Asp	Lys	Val	Leu	Ser	
287					925						930					935	
289	gtc	cac	aca	gac	cct	gtc	cac	ctc	tat	aag	aac	tgg	atc	aac	cag	act	3245
290	Val	His	Thr	Asp	Pro	Val	His	Leu	Tyr	Lys	Asn	Trp	Ile	Asn	Gln	Thr	
291					940						945					950	
293	gag	gcc	cag	aca	ggg	cag	cgc	agc	cat	ctc	cca	tat	gat	gtc	acc	ccg	3293
294	Glu	Ala	Gln	Thr	Gly	Gln	Arg	Ser	His	Leu	Pro	Tyr	Asp	Val	Thr	Pro	
295					955						960					965	
297	gag	cag	gcc	ttg	agc	cac	ccc	gag	gtc	cag	aga	cga	ctg	gac	atc	gcc	3341
298	Glu	Gln	Ala	Leu	Ser	His	Pro	Glu	Val	Gln	Arg	Arg	Leu	Asp	Ile	Ala	
299					970						975					980	
301	cta	cgc	aac	ctc	ctc	gcc	atg	act	gat	aag	ttc	ctt	tta	gcc	atc	acc	3389
302	Leu	Arg	Asn	Leu	Leu	Ala	Met	Thr	Asp	Lys	Phe	Leu	Leu	Ala	Ile	Thr	
303	985					990						995				1000	
305	tca	tct	gtg	gac	caa	att	ccg	tat	ggg	atg	cga	tat	gtg	gcc	aaa	gtc	3437
306	Ser	Ser	Val	Asp	Gln	Ile	Pro	Tyr	Gly	Met	Arg	Tyr	Val	Ala	Lys	Val	
307					1005						1010					1015	
309	ctg	aag	gca	act	ctg	gca	gag	aaa	ttc	cct	gac	gcc	aca	gac	agc	gag	3485
310	Leu	Lys	Ala	Thr	Leu	Ala	Glu	Lys	Phe	Pro	Asp	Ala	Thr	Asp	Ser	Glu	
311					1020					1025						1030	
313	gtc	tat	aag	gtg	gtc	ggg	aac	ctc	ctg	tac	tac	cgc	ttc	ctg	aac	cca	3533
314	Val	Tyr	Lys	Val	Val	Gly	Asn	Leu	Leu	Tyr	Tyr	Arg	Phe	Leu	Asn	Pro	
315					1035					1040						1045	
317	gct	gtg	gtg	gct	cct	gac	gcc	ttc	gac	att	gtg	gcc	atg	gca	gct	ggt	3581
318	Ala	Val	Val	Ala	Pro	Asp	Ala	Phe	Asp	Ile	Val	Ala	Met	Ala	Ala	Gly	
319					1050						1055					1060	
321	gga	gcc	ctg	gct	gcc	ccc	cag	cgc	cat	gcc	ctg	ggg	gct	gtg	gct	cag	3629
322	Gly	Ala	Leu	Ala	Ala	Pro	Gln	Arg	His	Ala	Leu	Gly	Ala	Val	Ala	Gln	
323	1065					1070					1075					1080	
325	ctc	cta	cag	cac	gct	gcg	gct	ggc	aag	gcc	ttc	tct	ggg	cag	agc	cag	3677

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L:7 M:270 C: Current Application Number differs, Replaced Current Application No

L:7 M:271 C: Current Filing Date differs, Replaced Current Filing Date